

## Fig. 1

Human glycoprotein hormone  $\beta$ 10 polypeptide:

MKLAFLFLGPNMALLLLAGYGCVLGASSCNLRTFVGCNREFTLAKKPGCRGLRITTDACWRCETWEKPILEPPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVVAIRCDGACSTATTEC

Nucleic acid encoding human glycoprotein hormone  $\beta$ 10 polypeptide:

ATGAAGCTGGCATTCCTCTTCTTGGCCCCCATGGCCCCCTCCTCCTTCTGGC  
TGGCTATGGCTGTGTCCTCGGTGCTCCAGTGGAAACCTGCGCACCTTTTG  
TGGCTGTGCCGTGAGGAGTTTACTTCTTGGCCAAAGCCAGGCTGC  
AGGGCCCTTCGGATCACACGGATGCTGCTGGGGTGGCTGTGAGACCTG  
GGAGAAACCCATTCTGGAAACCCCTATATTGAAGCCCATCATCGAGTCT  
GTACCTACAAACGAGACCAACAGGTGACTGTCAAGCTGCCCAACTGTGCC  
CCGGAGTCGACCCCTTCTACACCTATCCCGTGGCCATCCGCTGTGACTG  
CGGAGCCCTGCTCCACTGCCACCAACGGAGTGTGAGACCATCTGAGGCCGCT  
AGCTGCTCTCTGCAGACCCACCTGTGTGAGCAGCACATGC

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TO: HUMAN  $\beta$ 10      CHECK: 6611    FROM: 1    TO: 106

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	140	LENGTH:	129
RATIO:	1.321	GAPS:	4
PERCENT SIMILARITY:	47.368	<b>PERCENT IDENTITY:</b>	<b>36.842</b>

HUMAN TSH- $\beta$  X HUMAN  $\beta$ 10

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1 .....FCIPTEYTMHIERRECAAYCLTINTTICAGYCMTRDINGK 40
      | :| .: | | | | | | : :
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWE..KPI 47
.
41 FLPKYALSQD.VCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCGKCN 89
      | | . |||| : ||.:| | | |.:.||||: | || |.
48 LEPPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDCGACS 97
.
90 TDYSDCIHEAIKTN YCTKPQKSYLVGFSV 118
      | .:| | |
98 TATTEC..ETI..... 106

```

## Fig. 2B

GAP OF: HUMAN FSH- $\beta$  CHECK: 8841 FROM: 1 TO: 111  
 TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:  
 /GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
 COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	156	LENGTH:	122
RATIO:	1.472	GAPS:	3
PERCENT SIMILARITY:	44.211	<b>PERCENT IDENTITY:</b>	<b>35.789</b>

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):

	=	IDENTITY
:	=	2
.	=	1

HUMAN FSH- $\beta$  X HUMAN  $\beta$ 10

```

1 .....NSCELTNITIAIEKEECRFCISINTTWCAGYCYTRDL.VYK 40
      | . | . | | : | | | | | : : .
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWEKPILE 49

41 DPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTPVATQCHCGKCDS 90
      | : ||: | ||: . | | | | | | | . | | | .
50 PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYTPVAIRCDCGACSTA 99

91 STDC.TVRGLGPSYCSFGEMKE 111
      . | : | | :
100 TTECETI..... 106
```

T0220"456T860

## Fig. 2C

GAP OF: HUMAN LH- $\beta$  CHECK: 5679 FROM: 1 TO: 121

TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	140	LENGTH:	125
RATIO:	1.321	GAPS:	3
PERCENT SIMILARITY:	44.118	<b>PERCENT IDENTITY:</b>	<b>32.353</b>

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):

	=	IDENTITY
:	=	2
.	=	1

HUMAN LH- $\beta$  X HUMAN  $\beta$ 10

```

1  .SREPLRPW..CHPINAILAVEKEGCPVCITVNTTICAGYCPTMMR.VLQ 46
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1  ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWEKPILE 49

47  AVLPPPLPQVVCTYRDVRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRS 96
   |||| : : .::||| | |||| .:||||: | || | .
50  PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYTPVAIRCDGACSTA 99

97  TSDCGGPKDHPLTCDHPQLSGLLFL 121
   |.:|
100 TTECETI..... 106
  
```

0981394.0334

# Fig. 2D

GAP OF: HUMAN CG- $\beta$  CHECK: 2358 FROM: 1 TO: 145

TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHECK: 6430

GAP WEIGHT: 8 AVERAGE MATCH: 2.912  
LENGTH WEIGHT: 2 AVERAGE MISMATCH: -2.003

QUALITY: 131 LENGTH: 149  
RATIO: 1.236 GAPS: 3  
PERCENT SIMILARITY: 42.157 **PERCENT IDENTITY: 31.373**

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):  
| = IDENTITY  
: = 2  
. = 1

HUMAN CG- $\beta$  X HUMAN  $\beta$ 10

```

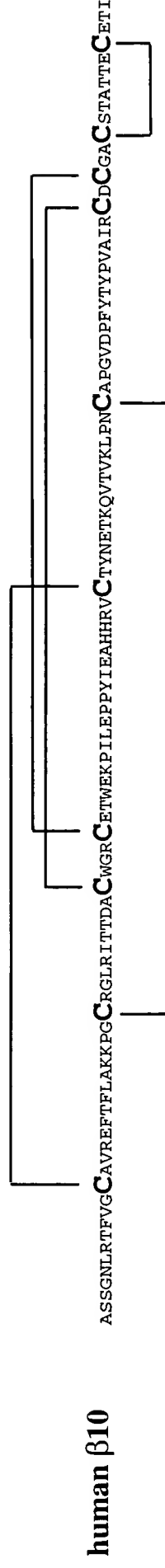
1 .SKEPLRP..RCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTR.VLQ 46
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEWEPKILE 49

47 GVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRS 96
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
50 PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDCGACSTA 99

97 TTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ 145
  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
100 TTECETI..... 106
  
```

09818954, 098204

**Fig. 3**



[illegible]

to: mouse  $\beta$ 10    check: 7740    from: 1    to: 106

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	577	Length:	106
Ratio:	5.443	Gaps:	0
Percent Similarity:	97.170	Percent Identity:	93.396

human  $\beta 10$  x mouse  $\beta 10$

[illegible]